International Journal of Ecology and Environmental Sciences
www.ecologyjournal.in
Online ISSN: 2664-7133; Print ISSN: 2664-7125; Impact Factor: RJIF 5.28
Received: 01-10-2020; Accepted: 15-10-2020; ; Published: 03-11-2020
Volume 2; Issue 4; 2020; Page No. 228-232

Assessment of genetic variability, heritability and genetic advance for yield and fruit traits in arecanut (*Areca Catechu* L.)

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Abstract

Arecanut is the high value commercial crop of coastal and malnad regions of India. India stands first in area and production. It is used for chewing purposes and also in Ayurveda and veterinary medicines. Partitioning of genetic variability into various components helps in understanding the genetic nature of yield and its components. The experiment was conducted at Agricultural and Horticultural Research Station, Sringeri, Karnataka, India, using 10 cultivars in a randomized block design to know the pattern and degree of genetic variability. The analysis of variance indicated a significant variation among genotypes for all the characters. The genotype Mangala recorded higher mean value for characters like fruit length, fruit breadth, husk thickness, fresh weight of husk, fresh nut yield, bunch weight, fresh weight of kernel, dry weight of kernel, fresh weight of husk per palm, dry weight of husk per palm and number of inflorescences. High estimates of PCV (%), GCV (%), heritability coupled with high genetic advance as per cent mean were observed among the characters. The higher value of PCV and GCV were observed for yield (81.26 per cent and 79.74 per cent), dry husk weight (69.93 per cent and 67.78 per cent) and fresh kernel weight (65.05 per cent and 64.03 per cent). Heritability estimates varied from 13.23 to 99.0 per cent. Hence, these characters were found highly influenced by the additive gene action and could be used in genetic improvement through direct selection.

Keywords: arecanut, GAM, GCV, heritability, PCV, variability

Introduction

Arecanut (Areca catechu L.) is a high value commercial crop of India, which is also called betel nut. The genus Areca belongs to the family Palmae (Arecaceae), which was first identified as monospecific (Areca catechu L.) in Linnaeus's Species Plantarum (1753). The genus expanded rapidly from its mono-specific status and at present the genus Areca had 76 species within the family. Among these, Areca catechu is the only cultivating species in the tribe Arecae. According to Watt (1889) [24], arecanut is a native of Cochin China and Malay Peninsula. It is also reported to be a native of Indonesia (Gode, 1961) [8]. The areca palm, a monocot plant and monoecious as well as it is a highly cross-pollinated crop. It is an allotetraploid with chromosome number 2n =32. The generic name Areca was coined by Linnaeus based on the popular Malayalam name 'Adeca' or a variant Kannada name as indicated by Bavappa (1964) [6]. Two wild species *viz*., Areca triandra and A. concinna are also used as masticatory (Kulkarni and Mulani, 2004) [12]. It is grown in India, Bangladesh, China, Malaysia, Indonesia, Vietnam, Philippines and Thailand. India stands first in the world in arecanut production followed by Myanmar, Bangladesh, China and Indonesia. (INDIASTAT, 2018). A total of 8.33 lakh tons of arecanut was produced from 4.97 lakh ha. In India with a productivity of 1676 kg per ha (INDIASTAT, 2018). Area and production in different states indicate that Karnataka, Kerala and Assam occupy 80 per cent of area and production followed by Meghalaya, West Bengal, Tamil Nadu, Mizoram and Odisha. The ultimate goal of any crop improvement programme is to improve the plant traits for agronomic and economic superiority, which depends largely on the magnitude of genetic variability and the extent to which the desirable trait is heritable. The estimates of variability for yield and its contributing characters and their heritable components in the material are more important in plant breeding programmes. Therefore, the present investigation was carried out to study the presence of genetic variability, heritability and genetic advance for thirty four quantitative traits among different arecanut genotypes.

Material and methods

The experiment was carried out at Agricultural and Horticultural Research Station, Sringeri, which is located in the Western Ghats and represents the typical hill zone (9) of Karnataka during Kharif 2018. The palms were planted with the spacing of 2.7 × 2.7 m. The experiment was laid out in Randomized Block Design with ten arecanut cultivars namely Sumangala, Sringeri local, Mohitnagar, SAS-1, Hirehalli Dwarf, Keladi Local, Sagar Local, Thirthahalli Local, Sreemangala and Mangala as test entries with three replications. Observations were recorded on stem girth, number of leaves, number of leaflets, length of leaf sheath, breadth of leaf sheath, plant height, crown shape, crown length, inter nodal length, number of fronds, length of oldest leaf, breadth of oldest leaf, total chlorophyll content, number of female flowers per inflorescence, number of nuts per inflorescence, total nuts per palm, color of ripe nuts, shape of nuts, fruit length, fruit breadth, fresh fruit weight, husk thickness, kernel length, fruit volume, kernel breadth, dry weight of kernel, fresh weight of husk, dry weight of husk, fresh nut yield, dry kernel weight, recovery percentage, bunch weight, Fresh kernel weight and yield. Variability parameters *viz.*, range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2), genetic advance (GA) and Genetic Advance as percent Mean (GAM) with respect to various morpho-physiological and yield characters in ten genotypes of arecanut were analyzed.

Results and Discussion

The analysis of variance showed significant differences among the genotypes for all the characters studied (Table 1 and 2). The extent of variability present in the germplasm provides scope for the crop improvement programme and also depends on the extent of heritability for a trait. Range of variation observed for all the traits indicated the presence of sufficient amount of variation among the genotypes for all the characters studied (Table 3 and 4). The genotype Mangala recorded higher mean value for traits like fruit length, fruit breadth, husk thickness, fresh weight of husk, fresh nut yield, bunch weight, fresh weight of kernel, dry weight of kernel, fresh weight of husk per palm, dry weight of husk per palm and number of inflorescences. SAS-1 recorded the lowest value for fruit length and kernel length. Sringeri Local recorded the lowest value for fruit breadth and fruit volume. Sumangala recorded higher value for fruit volume and lowest value for number of nuts per inflorescence. Mohitnagar recorded higher value for fresh fruit weight, kernel breadth, fresh weight of kernel, dry weight of kernel and dry weight of husk while lower value for recovery percentage. The minimum kernel weight was observed in Hirehalli Dwarf. The higher kernel weight was observed in Sumangala, Mohitnagar cultivars which has been reported earlier (Ananda and Rajesh, 2004) [2]. Phenotypic expression of any traits largely depends on the genotype of the plant and influences environmental variation but generally, higher environmental influence suppresses the complete expression of genes. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters studied (Table 3 and 4). In the present investigation, high estimates of GCV and PCV values were observed for Plant height (36.62 % and 30.81 %), inter nodal length (32.55 % and 26.41%), number of female flowers per inflorescence (49.70 % and 33.19 %), number of nuts per inflorescence (25.21 % and 24.20 %), total nuts per palm (30.61 % and 26.02 %), fresh fruit weight (27.34 % and 26.83 %), husk thickness (28.90 % and 28.26 %), fruit volume (40.36 % and 39.51 %), dry weight of kernel (37.0 % and 34.20 %), fresh kernel weight (23.91 % and 23.42 %), fresh weight of husk (31.60 % and 30.77%), dry weight of husk (32.80 % and 31.31 %), fresh nut yield (42.18 % and 41.16 %), Yield (81.26 % and 79.74 %), recovery percentage (31.77 % and 31.62 %), Bunch weight (44.55 % and 43.38 %), number of bunches per palm (67.54 % and 61.93 %). Ananda *et al.* (2000) [5] noticed the higher PCV and GCV for husk thickness, dry husk weight, dry kernel weight and dry fruit weight in arecanut varieties. Therefore, these characters offer good scope for further genetic improvement by recurrent selection similarly, high GCV for these traits also reported by Rao and Shrivastav, 1994 [16]; Sawant *et al.*, 1995 [20]; Roy *et al.*, 2001 [8]. High GCV and PCV values with narrow differences is an indication of the existence of a broad genetic base among the population, Suggesting stable expression of genotypes for these traits which provides scope for the improvement of these characters through simple selection. Moderate GCV and PCV were observed for stem girth (19.34 % and 10.06 %), fruit length (14.08 % and 13.90 %), fruit breadth (17.66 % and 17.28 %), kernel length (19.27 % and 19.14 %) which indicated the presence of moderate amount of variability for these traits and little influence of environment on these traits. These observations are in line with the findings of Ananda *et al.* (2000) [5]. Crown length and length of leaf sheath recorded moderate GCV (13.08 % and 19.01 %) and high PCV (26.17 % and 21.22 %) respectively, which indicates the considerable amount of genetic variability and less influence of non-genetic factors. The results obtained are in conformity with the findings of Ananda *et al.*, (2004) [2]. Moderate PCV and low GCV found in the number of leaves (14.52 % and 7.67 %), number of leaflets (16.58 % and 6.03 %), breadth of leaf sheath (15.63 % and 5.45 %). It showed less genetic variability for these characters. High differences in GCV and PCV were found for number of female flower (33.19, 49.70), number of leaves (7.67, 14.52), number of leaflets (6.03, 16.58), internodal length (26.41, 32.55), stem girth (10.06, 19.34), crown length (19.01, 26.17) and plant height (30.81, 36.62). The lower values of PCV and GCV indicated that such characters are highly susceptible for random environmental effects. It was observed that the genotypic coefficients of variation varied with the characters and this indicated the presence of genetic diversity for the different traits. High heritability coupled with high genetic advance as per cent mean was observed for recovery percentage (99.01 % and 64.89 %) followed by kernel length (98.71 and 39.18), fruit length (97.45 and 28.20), number of inflorescence, fresh weight of husk, fresh kernel weight, fresh fruit weight, dry kernel yield, fruit volume, fruit breadth, husk thickness, fresh weight of kernel, fresh nut weight, bunch weight, dry weight of husk, number of nuts per inflorescence and dry weight of husk for single fruit. The characters that endowed with high values may be used as selection criteria in genetic improvement of yield. High heritability for the traits have also reported by the earlier research reported by (Sarawgi and Soni, 1994 [19]; Reddy *et al.*, 1997; Roy *et al.*, 2001) [18]. Ananda *et al.* (2000) [5] reported higher heritability estimates for fresh fruit weight, dry kernel weight, and dry husk weight, suggesting the influence of both additive and non-additive gene effects in the expression of these traits. Similar results were obtained by Ananda *et al.* (2000) [5] that showed low narrow sense heritability for different traits studied thus indicating that non-additive effects play an important role in controlling the traits.

Table 1: Analysis of variance for thirteen quantitative growth parameters of Arecanut

Sources of variance	Replication	Varieties	CV	Error	CD@ 5%	CD@ 1%	S.Em±
Degrees of freedom	2	9					
plant height (m)	1.720	6.310**	19.80	0.760	1.490	2.050	0.470
Crown length (m)	0.190	0.300**	17.980	0.070	0.450	0.620	0.140

Girth (m)	6.18	26.41	9.77	4.780	3.750	5.140	1.260
Internodal length (m)	0.001	0.005**	19.020	0.0008	0.040	0.060	0.0150
No. Of fronds	0.500	4.950	16.430	1.450	2.070	2.830	0.70
No. Of leaflets	117.500	483.800	17.640	180.880	23.070	31.610	7.760
Length of oldest leaf (m)	0.210	0.350**	16.860	0.070	0.460	0.630	0.147
Breadth of oldest leaf (m)	0.210	0.240**	17.120	0.070	0.450	0.620	0.140
Length of leaf sheath (m)	0.060	0.060	16.700	0.020	0.250	0.340	0.080
Breadth of leaf sheath (m)	0.002	0.010	16.560	0.003	0.110	0.140	0.040
No. of bunches/ palm	0.070	0.630**	18.56	0.030	0.330	0.450	0.100
Total Chlorophyll (mg/ml)	305.100	5700.900**	7.660	1110.800	57.170	78.320	81.250
No. Of female flowers per inflorescence	5360.430	24859.900**	19.95	7279.390	146.350	200.510	46.730
Yield	1305405100	4433023	9.670	44480.580	361.780	495.670	115.510

*Level of significance at 5%**Level of significance at 1%

Table 2: Analysis of variance for twenty one yield attributing traits of Arecanut

Sources of variance	Replication	Varieties	CV	Error	CD@ 5%	CD@ 1%	Sem
Degrees of freedom	2	9					
Fruit length (cm)	140.67	730.32**	2.25	1.21	1.89	2.99	0.60
Fruit breadth (cm)	115.02	367502**	3.64	1.68	2.22	3.04	0.71
Fruit volume (cm^3)	19.90	32.39**	8.23	0.46	1.16	1.59	0.37
Fresh fruit weight (g)	232.42	315.97**	5.24	2.92	2.93	4.01	0.93
Husk thickness (mm)	3.95	4.69**	6.02	0.05	0.41	0.57	0.13
Kernel length (mm)	59.97	161.29**	2.19	0.26	0.87	1.19	0.27
Kernel breadth (mm)	11.94	166.86**	4.56	1.31	1.96	2.69	0.62
Fresh weight of kernel (g)	14.62	25.21**	4.81	0.20	0.77	1.05	0.24
Dry weight of kernel (g)	3.75	7.71**	13.95	0.40	1.08	1.49	0.34
Fresh weight of husk (g)	101.40	107.96**	7.19	1.81	2.31	3.16	0.73
Dry weight of husk (g)	4.15	5.23**	9.75	0.16	0.69	0.95	0.22
Fresh nut yield (g)	4891137	95537780**	9.25	158365	682.64	935.27	217.96
Bunch wt. (g)	12970.60	319015.80**	10.14	5707.42	129.59	177.55	41.37
Fresh kernel weight (g)	420710.30	1871482**	11.47	19807.39	241.42	330.76	77.08
Dry kernel wt.(g)	4433023	1305405100**	9.67	44480.58	361.78	495.67	115.51
Fresh husk (g)	434255.90	53221149**	17.18	9108.13	163.71	224.29	52.27
Dry husk (g)	0.60	0.95**	4.24	0	0.13	0.18	0.04
No. of inflorescence	815.80	1099.77**	7.06	22.55	8.14	11.16	2.60
No. Nuts per inflorescence	11.11	2168.38**	16.04	243.30	26.75	36.65	8.54
Total nuts per palm	5.44	944.62**	3.15	3.12	3.03	4.15	0.96
Recovery percentage (%)	117202.4	966178.1**	15.62	12201.81	189.48	259.60	60.5

*Level of significance at 5% **Level of significance at 1%

Table 3: Genetic variability for yield with thirteen quantitative traits of Arecanut

Sl. No.	Character	Mean ± SEM	Range		PCV (%)	GCV (%)	h^2 BS (%)	GAM (%)
			Min.	Max.				
1	Plant height (m)	4.41 ± 0.47	0.86	5.98	36.62	30.81	70.77	53.40
2	Crown length (m)	1.48 ± 0.14	0.66	1.84	26.17	19.01	52.78	28.45
3	Girth (m)	0.12 ± 0.01	0.10	0.15	19.34	10.06	53.01	0.12
4	Internodal length(m)	0.14 ± 0.01	0.03	0.18	32.55	26.41	65.83	44.14
5	No. Of fronds	7.32 ± 0.65	6.61	7.9	14.52	7.67	27.87	8.34
6	No. Of leaflets	76.22 ± 7.36	67.8	87.14	16.58	6.03	13.23	4.5
7	Length of oldest leaf (m)	1.6 ± 0.14	.7	1.88	25.52	19.15	56.32	29.60
8	Breadth of oldest leaf (m)	1.56 ± 0.14	0.81	1.85	23.05	15.44	44.87	21.31
9	Length of leaf sheath (m)	0.88 ± 0.08	0.52	1.02	21.22	13.08	38.0	16.61
10	Breadth of leaf sheath (m)	0.37 ± 0.03	0.33	0.43	15.63	5.45	12.18	3.92
11	No. of bunches/ palm	0.71 ± 0.10	0.29	1.4	67.54	61.93	81.09	116.99
12	Total Chlorophyll(mg/ml)	434.73± 18.25	353.39	504.38	11.82	8.99	57.94	14.10
13	No. Of female flowers per inflorescence	230.63 ± 46.73	67.66	360.66	49.70	33.19	44.60	45.66
14	Yield	1226.87±77.08	360	2675	65.05	64.03	96.89	129.84

Where Vp=Phenotypic variance PCV= Phenotypic coefficient of variation h2 BS=Heritability broad sense Vg=Genotypic variance GCV=Genotypic coefficient of variation GA=Genetic advance GAM=Genetic advance as per cent mean

Table 4: Genetic variability parameter of twenty one yield attributing traits of Arecanut

Sl. No.	Character	Mean± SEM	Range		PCV (%)	GCV (%)	h^2 BS (%)	GAM (%)
			Min.	Max.				
1	Fruit length (cm)	49.02± 0.6	40.51	57.5	14.08	13.90	97.45	28.20
2	Fruit breadth (cm)	35.50 ± 0.71	26.72	45.46	17.66	17.28	95.74	34.83
3	Fruit volume (cm^3)	8.25± 0.37	4	12.00	40.36	39.51	95.84	79.69
4	Fresh fruit weight (g)	32.59 ±0.93	18.41	45.76	27.34	26.83	96.32	54.24
5	Husk thickness (mm)	4.02± 0.13	2.36	6.70	28.90	28.26	95.65	56.94
6	Kernel length (mm)	23.30 ±0.27	17.95	33.94	19.27	19.14	98.71.	39.18
7	Kernel breadth (mm)	25.16 ±0.62	22.02	27.89	8.76	7.47	72.88	13.15
8	Fresh weight of kernel (g)	9.35± 0.24	5.45	13.10	23.91	23.42	95.65	47.27
9	Dry weight of kernel (g)	4.55 ±0.34	1.94	7.89	37.0	34.27	85.79	65.39
10	Fresh weight of husk (g)	18.71± 0.73	9.58	27.59	31.60	30.77	94.82	61.73
11	Dry weight of husk (g)	4.15± 0.22	2.16	6.40	32.8	31.31	91.16	61.60
12	Fresh nut yield (g)	4299.47 ±217.96	1660	6907	42.18	41.16	95.19	82.72
13	Bunch wt. (g)	744.85 ±41.37	302.0	1347.14	44.55	43.38	94.82	87.02
14	Fresh kernel weight(g)	1226.87 ±77.08	360.0	2675	65.05	64.03	96.89	129.84
15	Dry kernel wt.(g)	707.17 ±60.50	146.6	1920	81.26	79.74	96.30	161.20
16	Fresh husk (g)	2180.26 ±115.51	438.7	4301.4	56.31	55.47	97.05	112.57
17	Dry husk (g)	555.34 ±52.27	149.8	1476.6	69.93	67.78	93.96	135.35
18	No. of inflorescence	1.81± 0.042	1.00	2.42	25.00	24.64	97.12	50.82
19	No. Nuts per inflorescence	67.18± 2.60	33.5	87.1	25.21	24.20	92.14	47.85
20	Total nuts per palm	97.17± 8.54	65.88	145.80	30.61	26..02	72.52	45.73
21	Recovery percentage (%)	56.02 ±0.96	37.99	96.58	31.77	31.62	99.01	64.89

Where Vp =Phenotypic variance PCV= Phenotypic coefficient of variation h2 BS=Heritability broad sense Vg=Genotypic variance GCV=Genotypic coefficient of variation GA=Genetic advance GAM=Genetic advance as per cent mean

Conclusion

In the present investigation, high GCV and PCV were observed for the characters *viz.*, plant height, inter nodal length, number of female flowers per inflorescence, number of nuts per inflorescence, total nuts per palm, fresh fruit weight, husk thickness, fruit volume, dry weight of kernel, fresh kernel weight , fresh weight of husk, dry weight of husk, fresh nut yield, yield, recovery percentage, bunch weight, number of bunches per palm. Hence, these attributes can be improved through direct selection from the existing genotypes, as these characters have high degree of additive components of genetic variance.

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